

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Kossmann, Jens  
Willmitzer, Lothar  
Emmermann, Michael
- (ii) TITLE OF THE INVENTION: NUCLEIC ACID MOLECULES CODING FOR  
DEBRANCHING ENZYMES FROM MAIZE
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: FISH & NEAVE  
(B) STREET: 1251 Avenue of the Americas  
(C) CITY: New York  
(D) STATE: New York  
(E) COUNTRY: U.S.A.  
(F) ZIP: 10020-1104
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: PCT/EP97/01141  
(B) FILING DATE: 06-MAR-97
- (viii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: DE 196 08 918.2  
(B) FILING DATE: 07-MAR-96
- (ix) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Haley Jr., James F.  
(B) REGISTRATION NUMBER: 27,794  
(C) REFERENCE/DOCKET NUMBER: GFB-7
- (x) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (212) 596-9000  
(B) TELEFAX: (212) 596-9090

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1993 base pairs  
(B) TYPE: nucleotide  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Zea mays

(F) TISSUE TYPE: Blattgewebe

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..1675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

|   |     |
|---|-----|
| GGC ACG AGG TCA AAA CTC CCT CCA GGG TCA GAT TTG CAA CAA GCT GCA | 48  |
| Gly Thr Arg Ser Lys Leu Pro Pro Gly Ser Asp Leu Gln Gln Ala Ala |     |
| 1 5 10 15   |     |
| ATT GTG GCT ATT CAG GAA GAG GAC CCT TAT AAT TGG GGG TAT AAC CCT | 96  |
| Ile Val Ala Ile Gln Glu Glu Asp Pro Tyr Asn Trp Gly Tyr Asn Pro |     |
| 20 25 30  |     |
| GTG GTT TGG GGC GTT CCA AAA GGA AGC TAT GCA AGT AAC CCA GAT GGT | 144 |
| Val Val Trp Gly Val Pro Lys Gly Ser Tyr Ala Ser Asn Pro Asp Gly |     |
| 35 40 45  |     |
| CCA AGT CGT ATC ATT GAG TAC CGG CTG ATG GTG CAG GCC TTG AAT CGC | 192 |
| Pro Ser Arg Ile Ile Glu Tyr Arg Leu Met Val Gln Ala Leu Asn Arg |     |
| 50 55 60  |     |
| TTA GGT CTT CGA GTT GTC ATG GAT GTT GTA TAC AAT CAT CTA TAC TCA | 240 |
| Leu Gly Leu Arg Val Val Met Asp Val Val Tyr Asn His Leu Tyr Ser |     |
| 65 70 75 80   |     |
| AGT GGC CCT TTT GCC ATC ACT TCC GTG CTT GAC AAG ATT GTA CCT GGA | 288 |
| Ser Gly Pro Phe Ala Ile Thr Ser Val Leu Asp Lys Ile Val Pro Gly |     |
| 85 90 95  |     |
| TAC TAC CTC AGA AGG GAC TCT AAT GGT CAG ACT GAG AAC AGC GCG GCT | 336 |
| Tyr Tyr Leu Arg Arg Asp Ser Asn Gly Gln Thr Glu Asn Ser Ala Ala |     |
| 100 105 110   |     |
| GTG AAC AAT ACA GCA AGT GAG CAT TTC ATG GTT GAT AGA TTA ATC GTG | 384 |
| Val Asn Asn Thr Ala Ser Glu His Phe Met Val Asp Arg Leu Ile Val |     |
| 115 120 125   |     |
| GAT GAC CTT CTG AAT TGG GCA GTA AAT TAC AAA GTT GAC GGG TTC AGA | 432 |
| Asp Asp Leu Leu Asn Trp Ala Val Asn Tyr Lys Val Asp Gly Phe Arg |     |
| 130 135 140   |     |
| TTT GAT CTA ATG GGA CAT ATC ATG AAA AAG ACA ATG ATT AGA GCA AAA | 480 |
| Phe Asp Leu Met Gly His Ile Met Lys Lys Thr Met Ile Arg Ala Lys |     |
| 145 150 155 160   |     |
| TCG GCT CTT CAA AGC CTT ACA ATT GAT GAA CAT GGA GTA GAT GGT TCA | 528 |
| Ser Ala Leu Gln Ser Leu Thr Ile Asp Glu His Gly Val Asp Gly Ser |     |
| 165 170 175   |     |
| AAG ATA TAC TTG TAT GGT GAA GGA TGG AAC TTC GGT GAA GTT GCG GAA | 576 |
| Lys Ile Tyr Leu Tyr Gly Glu Gly Trp Asn Phe Gly Glu Val Ala Glu |     |
| 180 185 190   |     |
| AAT CAA CGT GGG ATA AAT GGA TCC CAG CTA AAT ATG AGT GGC ACT GGG | 624 |
| Asn Gln Arg Gly Ile Asn Gly Ser Gln Leu Asn Met Ser Gly Thr Gly |     |
| 195 200 205   |     |



|   |      |
|---|------|
| TTG GTT CCA GGA GTT ATT GTC ATG AGC ATC GAA GAT GCA CGA AAT GAT   | 1440 |
| Leu Val Pro Gly Val Ile Val Met Ser Ile Glu Asp Ala Arg Asn Asp   |      |
| 465 470 475 480   |      |
| AGG CAT GAT ATG GCC CAG ATA GAT GAA ACA TTC TCT TGT GTC GTT ACA   | 1488 |
| Arg His Asp Met Ala Gln Ile Asp Glu Thr Phe Ser Cys Val Val Thr   |      |
| 485 490 495   |      |
| GTC TTC AAT GTA TGT CCG TAC GAA GTG TCT ATA GAA ATC CCT GAT CTT   | 1536 |
| Val Phe Asn Val Cys Pro Tyr Glu Val Ser Ile Glu Ile Pro Asp Leu   |      |
| 500 505 510   |      |
| GCA TCA CTG CGG CTT CAG TTG CAT CCA GTG CAG GTG AAT TCA TCG GAT   | 1584 |
| Ala Ser Leu Arg Leu Gln Leu His Pro Val Gln Val Asn Ser Ser Asp   |      |
| 515 520 525   |      |
| GCG TTA GCC AGG CAG TCT GCG TAC GAC ACC GCC ACA GGT CGA TTC ACC   | 1632 |
| Ala Leu Ala Arg Gln Ser Ala Tyr Asp Thr Ala Thr Gly Arg Phe Thr   |      |
| 530 535 540   |      |
| GTG CCG AAA AGG ACA GCA GCA GTG TTC GTG GAA CCC AGG TGC T         | 1675 |
| Val Pro Lys Arg Thr Ala Ala Val Phe Val Glu Pro Arg Cys           |      |
| 545 550 555   |      |
| GATGGATGCC TTTCGCTAGC GAGCAAGTGC ATTCGGCATC CAAGTCGAAG CAAACGAATG | 1735 |
| AAATAAGAGA AGGCCATCGA ATAAAACGAA GTATATAAAT AGATTGAATA AGACGTTGCC | 1795 |
| CAAGTTGCCA AGGCACGCTT TGCCATATGT ATGCGTTGAA AAATAAATAA ATAAATAAAT | 1855 |
| AAATGATGTT ATAGAGGTAC AAAAGCATTG GAACATTTCT TTATAGAGGT GAACCACCCT | 1915 |
| ATTTTCCAGT TTCCATGTGT GAATTGTGAT TAGCATATGT ATGGAATAAT AATATAAATT | 1975 |
| AATTTTATGC AAAAAAAAAA   | 1993 |

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

|   |  |
|---|--|
| Gly Thr Arg Ser Lys Leu Pro Pro Gly Ser Asp Leu Gln Gln Ala Ala |  |
| 1 5 10 15   |  |
| Ile Val Ala Ile Gln Glu Glu Asp Pro Tyr Asn Trp Gly Tyr Asn Pro |  |
| 20 25 30  |  |
| Val Val Trp Gly Val Pro Lys Gly Ser Tyr Ala Ser Asn Pro Asp Gly |  |
| 35 40 45  |  |
| Pro Ser Arg Ile Ile Glu Tyr Arg Leu Met Val Gln Ala Leu Asn Arg |  |
| 50 55 60  |  |
| Leu Gly Leu Arg Val Val Met Asp Val Val Tyr Asn His Leu Tyr Ser |  |
| 65 70 75 80   |  |

Ser Gly Pro Phe Ala Ile Thr Ser Val Leu Asp Lys Ile Val Pro Gly  
 85 90 95  
 Tyr Tyr Leu Arg Arg Asp Ser Asn Gly Gln Thr Glu Asn Ser Ala Ala  
 100 105 110  
 Val Asn Asn Thr Ala Ser Glu His Phe Met Val Asp Arg Leu Ile Val  
 115 120 125  
 Asp Asp Leu Leu Asn Trp Ala Val Asn Tyr Lys Val Asp Gly Phe Arg  
 130 135 140  
 Phe Asp Leu Met Gly His Ile Met Lys Lys Thr Met Ile Arg Ala Lys  
 145 150 155 160  
 Ser Ala Leu Gln Ser Leu Thr Ile Asp Glu His Gly Val Asp Gly Ser  
 165 170 175  
 Lys Ile Tyr Leu Tyr Gly Glu Gly Trp Asn Phe Gly Glu Val Ala Glu  
 180 185 190  
 Asn Gln Arg Gly Ile Asn Gly Ser Gln Leu Asn Met Ser Gly Thr Gly  
 195 200 205  
 Ile Gly Ser Phe Asn Asp Arg Ile Arg Asp Ala Ile Asn Gly Gly Ser  
 210 215 220  
 Pro Phe Gly Asn Pro Leu Gln Gln Gly Phe Ser Thr Gly Leu Phe Leu  
 225 230 235 240  
 Glu Pro Asn Gly Phe Tyr Gln Gly Asn Glu Thr Glu Thr Arg Leu Thr  
 245 250 255  
 Leu Ala Thr Tyr Ala Asp His Ile Gln Ile Gly Leu Ala Gly Asn Leu  
 260 265 270  
 Lys Asp Tyr Val Val Ile Ser His Thr Gly Glu Ala Arg Lys Gly Ser  
 275 280 285  
 Glu Ile Arg Thr Phe Asp Gly Ser Pro Val Gly Tyr Ala Ser Ser Pro  
 290 295 300  
 Ile Glu Thr Ile Asn Tyr Ala Ser Ala His Asp Asn Glu Thr Leu Phe  
 305 310 315 320  
 Asp Ile Ile Ser Leu Lys Thr Pro Met Asp Leu Ser Ile Asp Glu Arg  
 325 330 335  
 Cys Arg Ile Asn His Leu Ser Thr Ser Met Ile Ala Leu Ser Gln Gly  
 340 345 350  
 Ile Pro Phe Phe His Ala Gly Asp Glu Ile Leu Arg Ser Lys Ser Leu  
 355 360 365  
 Asp Arg Asp Ser Tyr Asp Ser Gly Asp Trp Phe Asn Lys Ile Asp Phe  
 370 375 380  
 Thr Tyr Glu Thr Asn Asn Trp Gly Val Gly Leu Pro Pro Arg Glu Lys  
 385 390 395 400  
 Asn Glu Gly Ser Trp Pro Leu Met Lys Pro Arg Leu Glu Asn Pro Ser  
 405 410 415

Phe Lys Pro Ala Lys His Asp Ile Ile Ala Ala Leu Asp Lys Phe Ile  
 420 425 430  
 Asp Ile Leu Lys Ile Arg Tyr Ser Ser Pro Leu Phe Arg Leu Thr Thr  
 435 440 445  
 Ala Ser Asp Ile Val Gln Arg Val His Phe His Asn Thr Gly Pro Ser  
 450 455 460  
 Leu Val Pro Gly Val Ile Val Met Ser Ile Glu Asp Ala Arg Asn Asp  
 465 470 475 480  
 Arg His Asp Met Ala Gln Ile Asp Glu Thr Phe Ser Cys Val Val Thr  
 485 490 495  
 Val Phe Asn Val Cys Pro Tyr Glu Val Ser Ile Glu Ile Pro Asp Leu  
 500 505 510  
 Ala Ser Leu Arg Leu Gln Leu His Pro Val Gln Val Asn Ser Ser Asp  
 515 520 525  
 Ala Leu Ala Arg Gln Ser Ala Tyr Asp Thr Ala Thr Gly Arg Phe Thr  
 530 535 540  
 Val Pro Lys Arg Thr Ala Ala Val Phe Val Glu Pro Arg Cys  
 545 550 555

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE DESCRIPTION:
  - (A) LENGTH: 492 base pairs
  - (B) TYPE: nucleotide
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Solanum tuberosum
  - (B) STRAIN: Berolina
  - (F) TISSUE TYPE: tuber
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LAGE:1..492
  - (D) OTHER INFORMATION:/product= "debranching enzyme (R-enzyme) "

(xi) SEQUENCE INFORMATION: SEQ ID NO: 3:

|   |    |
|---|----|
| TCT GCT GAT GGC AAG TGG ACA TTA TTA GTT AAT CTT GAT TCT GAT GAT | 48 |
| Ser Ala Asp Gly Lys Trp Thr Leu Leu Val Asn Leu Asp Ser Asp Asp |    |
| 560 565 570   |    |
| GTA AAA CCT GAA GGC TGG GAT AAT CTA CAA GAC GTG AAG CCA AAT CTT | 96 |
| Val Lys Pro Glu Gly Trp Asp Asn Leu Gln Asp Val Lys Pro Asn Leu |    |
| 575 580 585 590   |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CTT | TCC | TTT | TCT | GAT | GTC | AGC | ATC | TAT | GAG | CTG | CAT | GTT | AGA | GAT | TTC | 144 |
| Leu | Ser | Phe | Ser | Asp | Val | Ser | Ile | Tyr | Glu | Leu | His | Val | Arg | Asp | Phe |     |
|     |     |     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| ACT | GCC | AGT | GAC | CCT | ACT | GTG | TCT | CAT | GAA | TTT | CAG | GCC | GGT | TAT | CTC | 192 |
| Thr | Ala | Ser | Asp | Pro | Thr | Val | Ser | His | Glu | Phe | Gln | Ala | Gly | Tyr | Leu |     |
|     |     |     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GCC | CCT | TCC | ACG | TCG | CAG | GCA | TCA | GCT | GGT | GTC | CAA | CAT | TTG | AAA | AGA | 240 |
| Ala | Pro | Ser | Thr | Ser | Gln | Ala | Ser | Ala | Gly | Val | Gln | His | Leu | Lys | Arg |     |
|     |     | 625 |     |     |     |     | 630 |     |     |     |     | 635 |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| TTA | TCA | AGT | GCT | GGT | ATC | ACT | CAT | GTC | CAC | CTG | TGG | CCA | ACC | TAT | CAA | 288 |
| Leu | Ser | Ser | Ala | Gly | Ile | Thr | His | Val | His | Leu | Trp | Pro | Thr | Tyr | Gln |     |
|     | 640 |     |     |     |     | 645 |     |     |     |     | 650 |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| TTT | GCT | GGT | GTC | GAA | GAT | GAG | AAA | CAT | AAA | TGG | AAG | TAT | ACA | GAT | ATC | 336 |
| Phe | Ala | Gly | Val | Glu | Asp | Glu | Lys | His | Lys | Trp | Lys | Tyr | Thr | Asp | Ile |     |
| 655 |     |     |     |     | 660 |     |     |     |     | 665 |     |     |     |     | 670 |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GAG | AAA | CTC | AAC | TCT | TTT | CCA | CCA | GAT | TCT | GAG | GAG | CAG | CAG | GCT | CTT | 384 |
| Glu | Lys | Leu | Asn | Ser | Phe | Pro | Pro | Asp | Ser | Glu | Glu | Gln | Gln | Ala | Leu |     |
|     |     |     | 675 |     |     |     |     |     | 680 |     |     |     |     | 685 |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| ATC | ACA | GCC | ATC | CAA | GAT | GAA | GAT | GGC | TAT | AAT | TGG | GGG | TAT | AAT | CCT | 432 |
| Ile | Thr | Ala | Ile | Gln | Asp | Glu | Asp | Gly | Tyr | Asn | Trp | Gly | Tyr | Asn | Pro |     |
|     |     |     | 690 |     |     |     |     | 695 |     |     |     |     | 700 |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GTT | CTC | TGG | GGA | GTT | CCA | AAG | GGA | AGC | TAT | GCT | GGT | AAT | GCA | AAT | GGT | 480 |
| Val | Leu | Trp | Gly | Val | Pro | Lys | Gly | Ser | Tyr | Ala | Gly | Asn | Ala | Asn | Gly |     |
|     |     | 705 |     |     |     |     | 710 |     |     |     |     | 715 |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| CCT | TGT | CGT | ATC |     |     |     |     |     |     |     |     |     |     |     |     | 492 |
| Pro | Cys | Arg | Ile |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     | 720 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser | Ala | Asp | Gly | Lys | Trp | Thr | Leu | Leu | Val | Asn | Leu | Asp | Ser | Asp | Asp |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Val | Lys | Pro | Glu | Gly | Trp | Asp | Asn | Leu | Gln | Asp | Val | Lys | Pro | Asn | Leu |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Leu | Ser | Phe | Ser | Asp | Val | Ser | Ile | Tyr | Glu | Leu | His | Val | Arg | Asp | Phe |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Thr | Ala | Ser | Asp | Pro | Thr | Val | Ser | His | Glu | Phe | Gln | Ala | Gly | Tyr | Leu |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Ala | Pro | Ser | Thr | Ser | Gln | Ala | Ser | Ala | Gly | Val | Gln | His | Leu | Lys | Arg |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |

Leu Ser Ser Ala Gly Ile Thr His Val His Leu Trp Pro Thr Tyr Gln  
                     85                    90                    95  
 Phe Ala Gly Val Glu Asp Glu Lys His Lys Trp Lys Tyr Thr Asp Ile  
                     100                    105                    110  
 Glu Lys Leu Asn Ser Phe Pro Pro Asp Ser Glu Glu Gln Gln Ala Leu  
                     115                    120                    125  
 Ile Thr Ala Ile Gln Asp Glu Asp Gly Tyr Asn Trp Gly Tyr Asn Pro  
                     130                    135                    140  
 Val Leu Trp Gly Val Pro Lys Gly Ser Tyr Ala Gly Asn Ala Asn Gly  
                     145                    150                    155                    160  
 Pro Cys Arg Ile

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